Amendments to the Specification:

Please substitute the following new title for the existing title:

Prognostic Evaluation of Cancer ~~Methods and Compositions for Treatment of Breast Cancer~~

Please substitute the following paragraph for the third full paragraph on page 15:

FIG. 8B. Alignment of the region of similarity between GRB-7 (SEQ ID NO:9) and F10E9.6 (SEQ ID NO:10). Alignment was performed using the GCG Bestfit program. Bold capital letters indicate identity and plain capital letters indicate conservative substitution, as defined by a score greater than 0.8 on the PAM 250 scoring table (Schwartz and Dayhoff, eds., 1979, Atlas of Protein Sequences and Structure, pp. 353-358, National Biomedical Research Foundation, Washington, D.C.)

Please substitute the following paragraph for the paragraph bridging pages 15-16:

FIG. 8C. Alignment of GRB-7 (SEQ ID NO:9) and F10E9.6 (SEQ ID NO:10) with the consensus sequences for pleckstrin domain. Bold capital letters indicate agreement with the consensus sequence as defined by both Mayer (SEQ ID NO:11) (Mayer et al., 1993, Cell, 73:629-630) and Haslam (SEQ ID NO:12) (Haslam et al., 1993, Nature, 363:309-310) while plain capital letters indicate agreement with only one of the consensus sequences. ϕ represents a hydrophobic residue, and Φ represents an aromatic residue.

Please substitute the following paragraph for the paragraph bridging pages 18-19:

The PTK components of the PTK/adaptor protein complexes of the invention are either cytoplasmic, intracellular, non-receptor PTKs or transmembrane, receptor-type PTKs or derivatives thereof, each of which comprises one or more characteristic peptide domains. Such domains may include one or more catalytic domains which may include, but are not limited to, a tyrosine kinase domain. A tyrosine kinase catalytic domain generally ranges in length from about 250 to about 300 amino acids, corresponding to a molecular weight of approximately 30 kDa. The location of the tyrosine kinase catalytic domain, while not fixed, is generally near the carboxyl terminus of its protein. Short, conserved, stretches of amino acid residues may be present within the tyrosine kinase domain, which alternate in sequence

with variable-length stretches of amino acid residues which do not exhibit a high level of conservation. The consensus sequences, corresponding to the most highly conserved of the tyrosine kinase catalytic domain amino acid residues have been compiled and are well known to those of ordinary skill in the art. See, for example, Hanks et al. (Hanks, S. K. et al., 1991, Science 241:42-52), and Wilks (Wilks, A. F., 1990, Prog. Growth Factor Res. 2:97-111) which are incorporated herein, by reference, in their entirety. Among such consensus sequences are the PTK-specific sequences D-L-R-A-A-N (SEQ ID NO:13) or D-L-A-A-R-N(SEQ ID NO:18), and P-I/V-K/R-W-T/M-A-P-E (SEQ ID NO:14). Moreover, see FIG. 1, for a diagram of some additional examples of such sequence motifs. In a preferred embodiment of the PTK/adaptor protein complexes of the invention, the PTK is the receptor PTK HER2. The HER2 tyrosine kinase catalytic domain is well known to those of skill in the art, see, for example, Plowman, G. et al., 1993, Proc. Natl. Acad. Sci. USA 90:1746-1750.

Please substitute the following paragraph for the paragraph bridging pages 19-20:

The PTK component of the PTK/adaptor protein complexes of the invention may further include one or more non-catalytic domains, which may include, but are not limited to, one or more SH2 and/or one or more SH3 domains, and/or (in the case of receptor PTKs) a hydrophobic transmembrane domain. An SH2 (i.e., src homology domain 2) non-catalytic domain is generally approximately 100 amino acid residues in length. Such SH2 domains may contain a number of highly conserved or invariant amino acid residues within several, preferably five, well-conserved amino acid sequence motifs, which are well known to those of ordinary skill in the art. See, for example Koch et al. (Koch, A. C., 1991, Science 252:668-674), which is incorporated herein, by reference, in its entirety. For example, the amino acid consensus sequences may include, but are not limited to, F-L-I-R-E-S (SEQ ID NO:19) and F-L- V-R-E-S (SEQ ID NO:20). The R residue of these consensus sequences is invariant among SH2 domains. Such well-conserved amino acid sequences motifs are separated by stretches of more variable amino acid sequence elements, which, while variable, generally contain one or more G or P residues.

Please substitute the following paragraph for the last full paragraph on page 27:

SH2 and SH3 peptide domains are as described, above, in Section 5.1. SH2-binding peptide domains are well known in the ala. See, for example, Songyang, S. et al. (Songyang, S. et al., 1993, Cell 72:767-778), Rotin et al. (Rotin, D. et al., EMBO J. 11:559-567), and Skolnick et al. (Skolnick, E. Y. et al., 1993, EMBO J. 12:1929-1936), which are incorporated herein, by reference, in their entirety. SH2 domains may exhibit a specificity for certain SH2-binding domains. For example, SH2-binding peptide domains may include, but are not limited to a phosphoTyr-hydrophilic-hydrophilic-Ile/Pro amino acid sequence motif (generally, such a sequence motif is preferred for SH2 domains of the type found in, for example, the src, fyn, Ick, fgr, abl, crk, and nck proteins), and phosphoTyr-hydrophobic-X-hydrophobic, and/or phosphotyr-Met-X-Met (generally, such sequence motifs are preferred for SH2 domains of the type found in, for example, p85, phospholipase C-.gammá., and SHPTP2 proteins). Further, a consensus sequence developed from the analysis of the domains of several proteins that bind the SH2 domains of the GRB-2 protein has been determined to be X-P-X-Y-V/I-N-V/I (SEQ ID NO:15). The tyrosine (Y) residue of such a consensus sequence is preferably phosphorylated. In addition, SH2-binding peptide domains may comprise regions rich in Ser and Thr residues some or all of which are phosphorylated (Pendergast, A. M. et al., 1991, Cell 66:161-171).